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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: LeukoSite, Inc.
- (B) STREET: 215 First Street
- (C) CITY: Cambridge
- (D) STATE/PROVINCE: Massachusetts
- (E) COUNTRY: U.S.A.
- (F) POSTAL CODE/ZIP: 02142
- (G) TELEPHONE: (617) 621-9350
- (I) TELEFAX: (617) 621-9349

(i) APPLICANT/INVENTOR:

- (A) NAME: Michael J. Briskin
- (B) STREET: 28 Harbell Street
- (C) CITY: Lexington
- (D) STATE/PROVINCE: Massachusetts
- (E) COUNTRY: U.S.A.
- (F) POSTAL CODE/ZIP: 02173

(i) APPLICANT/INVENTOR:

- (A) NAME: Douglas J. Ringler
- (B) STREET: 382 Ocean Avenue, #1008
- (C) CITY: Revere
- (D) STATE/PROVINCE: Massachusetts
- (E) COUNTRY: U.S.A.
- (F) POSTAL CODE/ZIP: 02151

(i) APPLICANT/INVENTOR:

- (A) NAME: Dominic Picarella
- (B) STREET: 2 North Bennet Court, #4
- (C) CITY: Boston
- (D) STATE/PROVINCE: Massachusetts
- (E) COUNTRY: U.S.A.
- (F) POSTAL CODE/ZIP: 02113

(i) APPLICANT/INVENTOR:

- (A) NAME: Walter Newman
- (B) STREET: 3 Durham Street, #3
- (C) CITY: Boston
- (D) STATE/PROVINCE: Massachusetts
- (E) COUNTRY: U.S.A.
- (F) POSTAL CODE/ZIP: 02115

(ii) TITLE OF INVENTION: Mucosal Vascular Addressins and Uses
Thereof

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
- (B) STREET: Two Militia Drive
- (C) CITY: Lexington
- (D) STATE: Massachusetts
- (E) COUNTRY: U.S.A.
- (F) ZIP: 02173-4799

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- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/523,004
 - (B) FILING DATE: 01-SEP-1995
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/386,857
 - (B) FILING DATE: 10-FEB-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brook, David E.
 - (B) REGISTRATION NUMBER: 22,592
 - (C) REFERENCE/DOCKET NUMBER: LKS94-04A2 PCT
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-861-6240
 - (B) TELEFAX: 617-861-9540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1624 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTT CTG GGG CTC CTC	48
Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu	
1 5 10 15	
CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG	96
Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu	
20 25 30	
CCG GTG GTG GCC GTG GCC TTG GGC GCC TCG CGC CAG CTC ACC TGC CGC	144
Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg	
35 40 45	

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CTG	GCC	TGC	GCG	GAC	CGC	GGG	GCC	TCG	GTG	CAG	TGG	CGG	GGC	CTG	GAC	192
Leu	Ala	Cys	Ala	Asp	Arg	Gly	Ala	Ser	Val	Gln	Trp	Arg	Gly	Leu	Asp	
50				55						60						
ACC	AGC	CTG	GGC	GCG	GTG	CAG	TCG	GAC	ACG	GGC	CGC	AGC	GTC	CTC	ACC	240
Thr	Ser	Leu	Gly	Ala	Val	Gln	Ser	Asp	Thr	Gly	Arg	Ser	Val	Leu	Thr	
65					70				75					80		
GTG	CGC	AAC	GCC	TCG	CTG	TCG	GGC	GCC	GGG	ACC	CGC	GTG	TGC	GTG	GGC	288
Val	Arg	Asn	Ala	Ser	Leu	Ser	Ala	Ala	Gly	Thr	Arg	Val	Cys	Val	Gly	
				85					90				95			
TCC	TGC	GGG	GCC	CGC	ACC	TTC	CAG	CAC	ACC	GTG	CAG	CTC	CTT	GTG	TAC	336
Ser	Cys	Gly	Gly	Arg	Thr	Phe	Gln	His	Thr	Val	Gln	Leu	Leu	Val	Tyr	
				100				105				110				
GCC	TTC	CCG	GAC	CAG	CTG	ACC	GTC	TCC	CCA	GCA	GCC	CTG	GTG	CCT	GGT	384
Ala	Phe	Pro	Asp	Gln	Leu	Thr	Val	Ser	Pro	Ala	Ala	Leu	Val	Pro	Gly	
				115				120				125				
GAC	CCG	GAG	GTG	GCC	TGT	ACG	GCC	CAC	AAA	GTC	ACG	CCC	GTG	GAC	CCC	432
Asp	Pro	Glu	Val	Ala	Cys	Thr	Ala	His	Lys	Val	Thr	Pro	Val	Asp	Pro	
				130				135				140				
AAC	GCG	CTC	TCC	TTC	TCC	CTG	CTC	GTC	GGG	GCC	CAG	GAA	CTG	GAG	GGG	480
Asn	Ala	Leu	Ser	Phe	Ser	Leu	Leu	Val	Gly	Gly	Gln	Glu	Leu	Glu	Gly	
				145				150			155		160			
GCG	CAA	GCC	CTG	GGC	CCG	GAG	GTG	CAG	GAG	GAG	GAG	GAG	CCC	CAG	528	
Ala	Gln	Ala	Leu	Gly	Pro	Glu	Val	Gln	Glu	Glu	Glu	Glu	Pro	Gln		
				165				170				175				
GGG	GAC	GAG	GAC	GTG	CTG	TTC	AGG	GTG	ACA	GAG	CGC	TGG	CGG	CTG	CCG	576
Gly	Asp	Glu	Asp	Val	Leu	Phe	Arg	Val	Thr	Glu	Arg	Trp	Arg	Leu	Pro	
				180				185				190				
CCC	CTG	GGG	ACC	CCT	GTC	CCG	CCC	GCC	CTC	TAC	TGC	CAG	GCC	ACG	ATG	624
Pro	Leu	Gly	Thr	Pro	Val	Pro	Pro	Pro	Ala	Leu	Tyr	Cys	Gln	Ala	Thr	Met
				195				200			205					
AGG	CTG	CCT	GGC	TTG	GAG	CTC	AGC	CAC	CGC	CAG	GCC	ATC	CCC	GTC	CTG	672
Arg	Leu	Pro	Gly	Leu	Glu	Leu	Ser	His	Arg	Gln	Ala	Ile	Pro	Val	Leu	
				210				215			220					
CAC	AGC	CCG	ACC	TCC	CCG	GAG	CCT	CCC	GAC	ACC	TCC	CCG	GAG	CCT	720	
His	Ser	Pro	Thr	Ser	Pro	Glu	Pro	Pro	Asp	Thr	Thr	Ser	Pro	Glu	Pro	
				225				230			235		240			
CCC	AAC	ACC	ACC	TCC	CCG	GAG	TCT	CCC	GAC	ACC	ACC	TCC	CCG	GAG	TCT	768
Pro	Asn	Thr	Thr	Ser	Pro	Glu	Ser	Pro	Asp	Thr	Thr	Ser	Pro	Glu	Ser	
				245				250			255					
CCC	GAC	ACC	ACC	TCC	CAG	GAG	CCT	CCC	GAC	ACC	ACC	TCC	CAG	GAG	CCT	816
Pro	Asp	Thr	Thr	Ser	Gln	Glu	Pro	Pro	Asp	Thr	Thr	Ser	Gln	Glu	Pro	
				260				265			270					
CCC	GAC	ACC	ACC	TCC	CAG	GAG	CCT	CCC	GAC	ACC	ACC	TCC	CCG	GAG	CCT	864
Pro	Asp	Thr	Thr	Ser	Gln	Glu	Pro	Pro	Asp	Thr	Thr	Ser	Pro	Glu	Pro	
				275				280			285					

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CCC GAC AAG ACC TCC CCG GAG CCC GCC CCC CAG CAG GGC TCC ACA CAC	912
Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His	
290 295 300	
ACC CCC AGG AGC CCA GGC TCC ACC AGG ACT CGC CGC CCT GAG ATC TCC	960
Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser	
305 310 315 320	
CAG GCT GGG CCC ACG CAG GGA GAA GTG ATC CCA ACA GGC TCG TCC AAA	1008
Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys	
325 330 335	
CCT GCG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC AGC AGT GCG GTG	1056
Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val	
340 345 350	
CTG GGA CTG CTG CTC CTG GCC TTG CCC ACG TAT CAC CTC TGG AAA CGC	1104
Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg	
355 360 365	
TGC CGG CAC CTG GCT GAG GAC GAC ACC CAC CCA CCA GCT TCT CTG AGG	1152
Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg	
370 375 380	
CTT CTG CCC CAG GTG TCG GCC TGG GCT GGG TTA AGG GGG ACC GGC CAG	1200
Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln	
385 390 395 400	
GTC GGG ATC AGC CCC TCC TGAGTGGCCA GCCTTTCCCC CTGTGAAAGC	1248
Val Gly Ile Ser Pro Ser	
405	
AAAAATAGCTT GGACCCCTTC AAGTTGAGAA CTGGTCAGGG CAAACCTGCC TCCCATTCTA	1308
CTCAAAAGTCA TCCCTCTGCT CACAGAGATG GATGCATGTT CTGATTGCCT CTTGGAGAA	1368
GCTCATCAGA AACTCAAAAG AAGGCCACTG TTTGTCTCAC CTACCCATGA CCTGAAGCCC	1428
CTCCCTGAGT GGTCCCCACC TTTCTGGACG GAACCACGTA CTTTTTACAT ACATTGATTC	1488
ATGTCTCACG TCTCCCTAAA AATGCGTAAG ACCAAGCTGT GCCCTGACCA CCCTGGGCC	1548
CTGTCGTCAAG GACCTCCTGA GGCTTTGGCA AATAAACCTC CTAAAATGAT AAAAAAAA	1608
AAAAAAAAA AAAAAAA	1624

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu	
1 5 10 15	

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Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu
20 25 30

Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg
35 40 45

Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp
50 55 60

Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr
65 70 75 80

Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
85 90 95

Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr
100 105 110

Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly
115 120 125

Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
130 135 140

Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
145 150 155 160

Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln
165 170 175

Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
180 185 190

Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met
195 200 205

Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu
210 215 220

His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
225 230 235 240

Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser
245 250 255

Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro
260 265 270

Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro
275 280 285

Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His
290 295 300

Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser
305 310 315 320

Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys
325 330 335

Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val
340 345 350

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Leu Gly Leu Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg
 355 360 365

Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg
 370 375 380

Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln
 385 390 395 400

Val Gly Ile Ser Pro Ser
 405

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTT CTG GGG CTC CTC	CTC	48
Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu		
1 5 10 15		
CTC GCC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG		96
Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu		
20 25 30		
CCG GTG GTG GCC GTG GCC TTG GGC GCC TCG CGC CAG CTC ACC TGC CGC		144
Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg		
35 40 45		
CTG GCC TGC GCG GAC CGC GGG GCC TCG GTG CAG TGG CGG GGC CTG GAC		192
Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp		
50 55 60		
ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC		240
Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr		
65 70 75 80		
GTC CGC AAC GCC TCG TCG GCG GCC GGG ACC CGC GTG TGC GTG GGC		288
Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly		
85 90 95		
TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CTT GTG TAC		336
Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr		
100 105 110		

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GCC	TTC	CCG	GAC	CAG	CTG	ACC	GTC	TCC	CCA	GCA	GCC	CTG	GTG	CCT	GGT	384
Ala	Phe	Pro	Asp	Gln	Leu	Thr	Val	Ser	Pro	Ala	Ala	Leu	Val	Pro	Gly	
115							120					125				
GAC	CCG	GAG	GTG	GCC	TGT	ACG	GCC	CAC	AAA	GTC	ACG	CCC	GTG	GAC	CCC	432
Asp	Pro	Glu	Val	Ala	Cys	Ser	Ala	His	Lys	Val	Thr	Pro	Val	Asp	Pro	
130							135					140				
AAC	GCG	CTC	TCC	TTC	TCC	CTG	CTC	GTC	GGG	GGC	CAG	GAA	CTG	GAG	GGG	480
Asn	Ala	Leu	Ser	Phe	Ser	Leu	Leu	Val	Gly	Gly	Gln	Glu	Leu	Glu	Gly	
145							150				155				160	
GCG	CAA	GCC	CTG	GGC	CCG	GAG	GTG	CAG	GAG	GAG	GAG	GAG	CCC	CAG	528	
Ala	Gln	Ala	Leu	Gly	Pro	Glu	Val	Gln	Glu	Glu	Glu	Glu	Pro	Gln		
							165		170				175			
GGG	GAC	GAG	GAC	GTG	CTG	TTC	AGG	GTG	ACA	GAG	CGC	TGG	CGG	CTG	CCG	576
Gly	Asp	Glu	Asp	Val	Leu	Phe	Arg	Val	Thr	Glu	Arg	Trp	Arg	Leu	Pro	
							180		185			190				
CCC	CTG	GGG	ACC	CCT	GTC	CCG	CCC	GCC	CTC	TAC	TGC	CAG	GCC	ACG	ATG	624
Pro	Leu	Gly	Thr	Pro	Val	Pro	Pro	Pro	Ala	Leu	Tyr	Cys	Gln	Ala	Thr	Met
							195		200			205				
AGG	CTG	CCT	GGC	TTG	GAG	CTC	AGC	CAC	CGC	CAG	GCC	ATC	CCC	GTC	CTG	672
Arg	Leu	Pro	Gly	Leu	Glu	Leu	Ser	His	Arg	Gln	Ala	Ile	Pro	Val	Leu	
							210		215			220				
CAC	AGC	CCG	ACC	TCC	CCG	GAG	CCT	CCC	GAC	ACC	ACC	TCC	CCG	GAG	TCT	720
His	Ser	Pro	Thr	Ser	Pro	Glu	Pro	Pro	Asp	Thr	Thr	Ser	Pro	Glu	Ser	
							225		230			235			240	
CCC	GAC	ACC	ACC	TCC	CCG	GAG	TCT	CCC	GAC	ACC	ACC	TCC	CAG	GAG	CCT	768
Pro	Asp	Thr	Thr	Ser	Pro	Glu	Ser	Pro	Asp	Thr	Thr	Ser	Gln	Glu	Pro	
							245		250			255				
CCC	GAC	ACC	ACC	TCC	CCG	GAG	CCT	CCC	GAC	AAG	ACC	TCC	CCG	GAG	CCC	816
Pro	Asp	Thr	Thr	Ser	Pro	Glu	Pro	Pro	Asp	Thr	Ser	Pro	Glu	Pro		
							260		265			270				
GCC	CCC	CAG	CAG	GGC	TCC	ACA	CAC	ACC	CCC	AGG	AGC	CCA	GGC	TCC	ACC	864
Ala	Pro	Gln	Gln	Gly	Ser	Thr	His	Thr	Pro	Arg	Ser	Pro	Gly	Ser	Thr	
							275		280			285				
AGG	ACT	CGC	CGC	CCT	GAG	ATC	TCC	CAG	GCT	GGG	CCC	ACG	CAG	GGA	GAA	912
Arg	Thr	Arg	Arg	Pro	Glu	Ile	Ser	Gln	Ala	Gly	Pro	Thr	Gln	Gly	Glu	
							290		295			300				
GTG	ATC	CCA	ACA	GGC	TCG	TCC	AAA	CCT	GCG	GGT	GAC	CAG	CTG	CCC	GCG	960
Val	Ile	Pro	Thr	Gly	Ser	Ser	Lys	Pro	Ala	Gly	Asp	Gln	Leu	Pro	Ala	
							305		310			315			320	
GCT	CTG	TGG	ACC	AGC	AGT	GCG	GTG	CTG	GGA	CTG	CTG	CTC	CTG	GCC	TTG	1008
Ala	Leu	Trp	Thr	Ser	Ser	Ala	Val	Leu	Gly	Leu	Leu	Leu	Leu	Ala	Leu	
							325		330			335				
CCC	ACC	TAT	CAC	CTC	TGG	AAA	CGC	TGC	CGG	CAC	CTG	GCT	GAG	GAC	GAC	1056
Pro	Thr	Tyr	His	Leu	Trp	Lys	Arg	Cys	Arg	His	Leu	Ala	Glu	Asp	Asp	
							340		345			350				

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ACC CAC CCA CCA GCT TCT CTG AGG CTT CTG CCC CAG GTG TCG GCC TGG	1104
Thr His Pro Pro Ala Ser Leu Arg Leu Leu Pro Gln Val Ser Ala Trp	
355 360 365	
GCT GGG TTA AGG GGG ACC GGC CAG GTC GGG ATC AGC CCC TCC	1146
Ala Gly Leu Arg Gly Thr Gly Gln Val Gly Ile Ser Pro Ser	
370 375 380	
TGAGTGGCCA GCCTTCCCC CTGTGAAAGC AAAATAGCTT GGACCCCTTC AAGTTGAGAA	1206
CTGGTCAGGG CAAACCTGCC TCCCATTCTA CTCAAAGTCA TCCCTCTGTT CACAGAGATG	1266
GATGCATGTT CTGATTGCCT CTTGGAGAA GCTCATCAGA AACTCAAAAG AAGGCCACTG	1326
TTTGTCTCAC CTACCCATGA CCTGAAGCCC CTCCCTGAGT GGTCCCCACC TTTCTGGACG	1386
GAACCACGTA CTTTTACAT ACATTGATTC ATGTCTCACG TCTCCCTAAA AATGCGTAAG	1446
ACCAAGCTGT GCCCTGACCA CCCTGGGCCCT GTGCGTCAG GACCTCCTGA GGCTTGGCA	1506
AATAAACCTC CTAAAATGAA AAAAAAAA AAA	1539

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu	
1 5 10 15	
Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu	
20 25 30	
Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg	
35 40 45	
Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp	
50 55 60	
Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr	
65 70 75 80	
Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly	
85 90 95	
Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr	
100 105 110	
Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly	
115 120 125	

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Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro
 130 135 140
 Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly
 145 150 155 160
 Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln
 165 170 175
 Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro
 180 185 190
 Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met
 195 200 205
 Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu
 210 215 220

 His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Ser
 225 230 235 240
 Pro Asp Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Gln Glu Pro
 245 250 255
 Pro Asp Thr Thr Ser Pro Glu Pro Pro Asp Lys Thr Ser Pro Glu Pro
 260 265 270
 Ala Pro Gln Gln Gly Ser Thr His Thr Pro Arg Ser Pro Gly Ser Thr
 275 280 285
 Arg Thr Arg Arg Pro Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu
 290 295 300
 Val Ile Pro Thr Gly Ser Ser Lys Pro Ala Gly Asp Gln Leu Pro Ala
 305 310 315 320
 Ala Leu Trp Thr Ser Ser Ala Val Leu Gly Leu Leu Leu Leu Ala Leu
 325 330 335
 Pro Thr Tyr His Leu Trp Lys Arg Cys Arg His Leu Ala Glu Asp Asp
 340 345 350
 Thr His Pro Pro Ala Ser Leu Arg Leu Leu Pro Gln Val Ser Ala Trp
 355 360 365
 Ala Gly Leu Arg Gly Thr Gly Gln Val Gly Ile Ser Pro Ser
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1721 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 4..1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGC ATG GAT CGG GGC CTG GCC CTC CTG CTG GCG GGG CTT CTG GGG CTC Met Asp Arg Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu	48
1 5 10 15	
CTC CAG CCG GGC TGC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG Leu Gln Pro Gly Cys Gln Ser Leu Gln Val Lys Pro Leu Gln Val	96
20 25 30	
GAG CCC CCG GAG CCG GTG GTG GCC GTG GCC CTG GGC GCC TCT CGC CAG Glu Pro Pro Glu Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln	144
35 40 45	
CTC ACC TGC CGC CTG GAC TGC GCG GAC CGC GGG GCC ACG GTG CAG TGG Leu Thr Cys Arg Leu Asp Cys Ala Asp Arg Gly Ala Thr Val Gln Trp	192
50 55 60	
CGG GGC CTG GAC ACC AGC CTG GGC GCG GTG CAG TCG GAC GCG GGC CGC Arg Gly Leu Asp Thr Ser Leu Gly Ala Val Gln Ser Asp Ala Gly Arg	240
65 70 75	
AGC GTC CTC ACC GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGT Ser Val Leu Thr Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg	288
80 85 90 95	
GTG TGC GTG GGC TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CGG Val Cys Val Gly Ser Cys Gly Arg Thr Phe Gln His Thr Val Arg	336
100 105 110	
CTC CTT GTG TAC GCC TTC CCG GAC CAG CTG ACC ATC TCC CCG GCA GCC Leu Leu Val Tyr Ala Phe Pro Asp Gln Leu Thr Ile Ser Pro Ala Ala	384
115 120 125	
CTG GTG CCT GGT GAC CCG GAG GTG GCC TGT ACG GCC CAC AAA GTC ACG Leu Val Pro Gly Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr	432
130 135 140	
CCT GTG GAC CCC AAT GCG CTC TCC TTC TCC CTG CTC CTG GGG GAC CAG Pro Val Asp Pro Asn Ala Leu Ser Phe Ser Leu Leu Leu Gly Asp Gln	480
145 150 155	
GAA CTG GAG GGG GCC CAG GCT CTG GGC CCG GAG GTG GAG GAG GAG GAG Glu Leu Glu Gly Ala Gln Ala Leu Gly Pro Glu Val Glu Glu Glu Glu	528
160 165 170 175	
GAG GAG CCC CAG GAG GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC Glu Glu Pro Gln Glu Glu Asp Val Leu Phe Arg Val Thr Glu Arg	576
180 185 190	
TGG CGG CTG CCG ACC CTG GCA ACC CCT GTC CTG CCC GCG CTC TAC TGC Trp Arg Leu Pro Thr Leu Ala Thr Pro Val Leu Pro Ala Leu Tyr Cys	624
195 200 205	

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Arg Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu
1 5 10 15

Gln Pro Gly Cys Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu
20 25 30

Pro Pro Glu Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu
35 40 45

Thr Cys Arg Leu Asp Cys Ala Asp Arg Gly Ala Thr Val Gln Trp Arg
50 55 60

Gly Leu Asp Thr Ser Leu Gly Ala Val Gln Ser Asp Ala Gly Arg Ser
65 70 75 80

Val Leu Thr Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val
85 90 95

Cys Val Gly Ser Cys Gly Arg Thr Phe Gln His Thr Val Arg Leu
100 105 110

Leu Val Tyr Ala Phe Pro Asp Gln Leu Thr Ile Ser Pro Ala Ala Leu
115 120 125

Val Pro Gly Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro
130 135 140

Val Asp Pro Asn Ala Leu Ser Phe Ser Leu Leu Gly Asp Gln Glu
145 150 155 160

Leu Glu Gly Ala Gln Ala Leu Gly Pro Glu Val Glu Glu Glu Glu
165 170 175

Glu Pro Gln Glu Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp
180 185 190

Arg Leu Pro Thr Leu Ala Thr Pro Val Leu Pro Ala Leu Tyr Cys Gln
195 200 205

Ala Thr Met Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile
210 215 220

Pro Val Leu His Gly Pro Thr Ser Arg Glu Pro Pro Asp Thr Thr Ser
225 230 235 240

Pro Glu Pro Arg Ala Ala Thr Ser Pro Glu Thr Thr Pro Gln Gln Gly
245 250 255

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Ser Thr His Ser Pro Arg Ser Pro Gly Ser Thr Arg Thr Cys Arg Pro
 260 265 270
 Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly
 275 280 285
 Ser Ser Lys Pro Thr Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser
 290 295 300
 Ser Ala Val Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu
 305 310 315 320
 Trp Lys Arg Cys Arg His Leu Ala Glu Asp Gly Ala His Pro Pro Ala
 325 330 335
 Ser Leu Ser Ser Gln Pro Phe Pro Leu
 340 345

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCTACTGCC AGGCCACG

18

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCCTGGGAG ATCTCAGGG

19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCACGATGA GGCTGCCTGG

20

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGGAGCCTG GGCTCCTGGG

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAAGCTTCC ACCATGGATT TCGGACTGGC CC

32

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGACTAGTG TCGGGCTGTG CAGGAC

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGACTAGTGG TTTGGACGAG CCTGTTG

27